

SEQUENCE LISTING

<110> Jomaa, Hassan

<120> Process for identifying chemical active ingredients and  
active ingredients for inhibiting the  
1-deoxy-D-xylulose-5-phosphate biosynthesis pathway

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<140> PCT/EP99/02463

<141> 1999-04-13

<150> DE19843279.8

<151> 1998-09-22

<150> DE19816196.4

<151> 1998-04-14

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<151> 1998-06-24

<150> DE19825585.3

<151> 1998-06-09

<150> DE19831637.2

<151> 1998-07-15

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<151> 1998-07-15

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<170> PatentIn Ver. 2.1

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ttg ttc gat ata gga aat gat gat aat aga aat acg aca tat ggc tat 362

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Tyr Ser Asn Lys Leu Tyr Met Asp Lys Arg Lys Asn Ile Asn Asn Val

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Lys Tyr Ser Glu Glu Tyr Met Asp Asp Asp Asn Phe Ile Lys Ser Phe	
1025 1030 1035	
att gga aaa tct aga att att aaa atg gat aat gaa aat aat aat aca	3290
Ile Gly Lys Ser Arg Ile Ile Lys Met Asp Asn Glu Asn Asn Asn Thr	
1040 1045 1050 1055	
aat gaa cat tat tca agc aga gga gat aca cag aca aaa aaa aaa aaa	3338
Asn Glu His Tyr Ser Ser Arg Gly Asp Thr Gln Thr Lys Lys Lys Lys	
1060 1065 1070	
gtt tgt atc ttt aac atg ggt agt atg ctt ttt aat gta att aat gct	3386
Val Cys Ile Phe Asn Met Gly Ser Met Leu Phe Asn Val Ile Asn Ala	
1075 1080 1085	

ata aaa gaa att gaa aaa gaa caa tat att tca cat aat tat tct ttt 3434  
 Ile Lys Glu Ile Glu Lys Glu Gln Tyr Ile Ser His Asn Tyr Ser Phe  
 1090 1095 1100

tca att gtt gat atg ata ttt tta aat cct tta gat aaa aat atg ata 3482  
 Ser Ile Val Asp Met Ile Phe Leu Asn Pro Leu Asp Lys Asn Met Ile  
 1105 1110 1115

gat cat gta ata aaa caa aat aaa cat caa tat tta att act tat gaa 3530  
 Asp His Val Ile Lys Gln Asn Lys His Gln Tyr Leu Ile Thr Tyr Glu  
 1120 1125 1130 1135

gat aat act ata ggt ggt ttt tct aca cat ttc aat aat tat tta ata 3578  
 Asp Asn Thr Ile Gly Gly Phe Ser Thr His Phe Asn Asn Tyr Leu Ile  
 1140 1145 1150

gaa aat aat tat att aca aaa cat aac tta tat gtt cat aat att tat 3626  
 Glu Asn Asn Tyr Ile Thr Lys His Asn Leu Tyr Val His Asn Ile Tyr  
 1155 1160 1165

tta tct aat gag cca att gaa cat gca tct ttt aag gat caa caa gaa 3674  
 Leu Ser Asn Glu Pro Ile Glu His Ala Ser Phe Lys Asp Gln Gln Glu  
 1170 1175 1180

gtc gtc aaa atg gat aaa tgt agt ctt gtc aat aga att aaa aat tat 3722  
 Val Val Lys Met Asp Lys Cys Ser Leu Val Asn Arg Ile Lys Asn Tyr  
 1185 1190 1195

ctt aaa aat aat cct aca tgatgtaaga taaatatata tttctaaaat 3770  
 Leu Lys Asn Asn Pro Thr  
 1200 1205

tatattttttt ttatacttta atgtgtacaa taaaatatat atctaaatat attttatttg 3830

tacgctttttt tttttttttt ttttaattggtt atttttgtat at 3872

<210> 4  
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 <213> Plasmodium falciparum

<400> 4  
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 1 5 10 15  
 Tyr Ile Leu Leu Ile Ile Tyr Ile Asn Leu Asn Gly Met Asn Asn Lys  
 20 25 30

Asn Gln Ile Lys Thr Glu Lys Ile Tyr Ile Lys Lys Leu Asn Arg Leu  
 35 40 45

Ser Arg Lys Asn Ser Leu Cys Ser Ser Lys Asn Lys Ile Ala Cys Leu  
 50 55 60

Phe Asp Ile Gly Asn Asp Asp Asn Arg Asn Thr Thr Tyr Gly Tyr Asn  
 65 70 75 80

Val Asn Val Lys Asn Asp Asp Ile Asn Ser Leu Leu Lys Asn Asn Tyr  
 85 90 95

Ser Asn Lys Leu Tyr Met Asp Lys Arg Lys Asn Ile Asn Asn Val Ile  
 100 105 110

Ser Thr Asn Lys Ile Ser Gly Ser Ile Ser Asn Ile Cys Ser Arg Asn  
 115 120 125

Gln Lys Glu Asn Glu Gln Lys Arg Asn Lys Gln Arg Cys Leu Thr Gln  
 130 135 140

Cys His Thr Tyr Asn Met Ser His Glu Gln Asp Lys Leu Ala Asn Asp  
 145 150 155 160

Asn Asn Arg Asn Asn Lys Lys Asn Phe Asn Leu Leu Phe Ile Asn Tyr  
 165 170 175

Phe Asn Leu Lys Arg Met Lys Asn Ser Leu Leu Asn Lys Asp Asn Phe  
 180 185 190

Phe Tyr Cys Lys Glu Lys Lys Leu Ser Phe Leu His Lys Ala Tyr Lys  
 195 200 205

Lys Lys Asn Cys Thr Phe Gln Asn Tyr Ser Leu Lys Arg Lys Ser Asn  
 210 215 220

Arg Asp Ser His Lys Leu Phe Ser Gly Glu Phe Asp Asp Tyr Thr Asn  
 225 230 235 240

Asn Asn Ala Leu Tyr Glu Ser Glu Lys Lys Glu Tyr Ile Thr Leu Asn  
 245 250 255

Asn Asn Asn Lys Asn Asn Asn Asn Lys Asn Asn Asp Asn Lys Asn Asn  
 260 265 270

Asp Asn Asn Asp Tyr Asn Asn Asn Asn Ser Cys Asn Asn Leu Gly Glu  
 275 280 285

Arg Ser Asn His Tyr Asp Asn Tyr Gly Gly Asp Asn Asn Asn Pro Cys  
 290 295 300

Asn Asn Asn Asn Asp Lys Tyr Asp Ile Gly Lys Tyr Phe Lys Gln Ile  
 305 310 315 320

Asn Thr Phe Ile Asn Ile Asp Glu Tyr Lys Thr Ile Tyr Gly Asp Glu  
 325 330 335

Ile Tyr Lys Glu Ile Tyr Glu Leu Tyr Val Glu Arg Asn Ile Pro Glu  
 340 345 350

Tyr Tyr Glu Arg Lys Tyr Phe Ser Glu Asp Ile Lys Lys Ser Val Leu  
 355 360 365

Phe Asp Ile Asp Lys Tyr Asn Asp Val Glu Phe Glu Lys Ala Ile Lys  
 370 375 380

Glu Glu Phe Ile Asn Asn Gly Val Tyr Ile Asn Asn Ile Asp Asn Thr  
 385 390 395 400

Tyr Tyr Lys Lys Glu Asn Ile Leu Ile Met Lys Lys Ile Leu His Tyr  
 405 410 415

Phe Pro Leu Leu Lys Leu Ile Asn Asn Pro Ser Asp Leu Lys Lys Leu  
 420 425 430

Lys Lys Gln Tyr Leu Pro Leu Leu Ala His Glu Leu Lys Ile Phe Leu  
 435 440 445

Phe Phe Ile Val Asn Ile Thr Gly Gly His Phe Ser Ser Val Leu Ser  
 450 455 460

Ser Leu Glu Ile Gln Leu Leu Leu Tyr Ile Phe Asn Gln Pro Tyr  
 465 470 475 480

Asp Asn Val Ile Tyr Asp Ile Gly His Gln Ala Tyr Val His Lys Ile  
 485 490 495

Leu Thr Gly Arg Lys Leu Leu Phe Leu Ser Leu Arg Asn Lys Lys Gly  
 500 505 510

Ile Ser Gly Phe Leu Asn Ile Phe Glu Ser Ile Tyr Asp Lys Phe Gly  
 515 520 525

Ala Gly His Ser Ser Thr Ser Leu Ser Ala Ile Gln Gly Tyr Tyr Glu  
 530 535 540

Ala Glu Trp Gln Val Lys Asn Lys Glu Lys Tyr Gly Asn Gly Asp Ile  
 545 550 555 560

Glu Ile Ser Asp Asn Ala Asn Val Thr Asn Asn Glu Arg Ile Phe Gln  
 565 570 575

Lys Gly Ile His Asn Asp Asn Asn Ile Asn Asn Asn Ile Asn Asn Asn  
 580 585 590

Asn Tyr Ile Asn Pro Ser Asp Val Val Gly Arg Glu Asn Thr Asn Val  
 595 600 605

Pro Asn Val Arg Asn Asp Asn His Asn Val Asp Lys Val His Ile Ala  
 610 615 620

Ile Ile Gly Asp Gly Gly Leu Thr Gly Gly Met Ala Leu Glu Ala Leu  
 625 630 635 640

Asn Tyr Ile Ser Phe Leu Asn Ser Lys Ile Leu Ile Ile Tyr Asn Asp  
 645 650 655

Asn Gly Gln Val Ser Leu Pro Thr Asn Ala Val Ser Ile Ser Gly Asn  
 660 665 670

Arg Pro Ile Gly Ser Ile Ser Asp His Leu His Tyr Phe Val Ser Asn  
 675 680 685

Ile Glu Ala Asn Ala Gly Asp Asn Lys Leu Ser Lys Asn Ala Lys Glu  
 690 695 700

Asn Asn Ile Phe Glu Asn Leu Asn Tyr Asp Tyr Ile Gly Val Val Asn  
 705 710 715 720

Gly Asn Asn Thr Glu Glu Leu Phe Lys Val Leu Asn Asn Ile Lys Glu  
 725 730 735

Asn Lys Leu Lys Arg Ala Thr Val Leu His Val Arg Thr Lys Lys Ser  
 740 745 750

Asn Asp Phe Ile Asn Ser Lys Ser Pro Ile Ser Ile Leu His Ser Ile  
 755 760 765

Lys Lys Asn Glu Ile Phe Pro Phe Asp Thr Thr Ile Leu Asn Gly Asn  
 770 775 780

Ile His Lys Glu Asn Lys Ile Glu Glu Glu Lys Asn Val Ser Ser Ser  
 785 790 795 800



Thr	Lys	Tyr	Asp	Val	Asn	Asn	Lys	Asn	Asn	Lys	Asn	Asn	Asp	Asn	Ser		805	810	815	
Glu	Ile	Ile	Lys	Tyr	Glu	Asp	Met	Phe	Ser	Lys	Glu	Thr	Phe	Thr	Asp		820	825	830	
Ile	Tyr	Thr	Asn	Glu	Met	Leu	Lys	Tyr	Leu	Lys	Lys	Asp	Arg	Asn	Ile		835	840	845	
Ile	Phe	Leu	Ser	Pro	Ala	Met	Leu	Gly	Gly	Ser	Gly	Leu	Val	Lys	Ile		850	855	860	
Ser	Glu	Arg	Tyr	Pro	Asn	Asn	Val	Tyr	Asp	Val	Gly	Ile	Ala	Glu	Gln		865	870	875	880
His	Ser	Val	Thr	Phe	Ala	Ala	Ala	Met	Ala	Met	Asn	Lys	Lys	Leu	Lys		885	890	895	
Ile	Gln	Leu	Cys	Ile	Tyr	Ser	Thr	Phe	Leu	Gln	Arg	Ala	Tyr	Asp	Gln		900	905	910	
Ile	Ile	His	Asp	Leu	Asn	Leu	Gln	Asn	Ile	Pro	Leu	Lys	Val	Ile	Ile		915	920	925	
Gly	Arg	Ser	Gly	Leu	Val	Gly	Glu	Asp	Gly	Ala	Thr	His	Gln	Gly	Ile		930	935	940	
Tyr	Asp	Leu	Ser	Tyr	Leu	Gly	Thr	Leu	Asn	Asn	Ala	Tyr	Ile	Ile	Ser		945	950	955	960
Pro	Ser	Asn	Gln	Val	Asp	Leu	Lys	Arg	Ala	Leu	Arg	Phe	Ala	Tyr	Leu		965	970	975	
Asp	Lys	Asp	His	Ser	Val	Tyr	Ile	Arg	Ile	Pro	Arg	Met	Asn	Ile	Leu		980	985	990	
Ser	Asp	Lys	Tyr	Met	Lys	Gly	Tyr	Leu	Asn	Ile	His	Met	Lys	Asn	Glu		995	1000	1005	
Ser	Lys	Asn	Ile	Asp	Val	Asn	Val	Asp	Ile	Asn	Asp	Asp	Val	Asp	Lys		1010	1015	1020	
Tyr	Ser	Glu	Glu	Tyr	Met	Asp	Asp	Asp	Asn	Phe	Ile	Lys	Ser	Phe	Ile		1025	1030	1035	1040
Gly	Lys	Ser	Arg	Ile	Ile	Lys	Met	Asp	Asn	Glu	Asn	Asn	Asn	Thr	Asn		1045	1050	1055	

Glu His Tyr Ser Ser Arg Gly Asp Thr Gln Thr Lys Lys Lys Lys Val  
1060 1065 1070

Cys Ile Phe Asn Met Gly Ser Met Leu Phe Asn Val Ile Asn Ala Ile  
1075 1080 1085

Lys Glu Ile Glu Lys Glu Gln Tyr Ile Ser His Asn Tyr Ser Phe Ser  
1090 1095 1100

Ile Val Asp Met Ile Phe Leu Asn Pro Leu Asp Lys Asn Met Ile Asp  
1105 1110 1115 1120

His Val Ile Lys Gln Asn Lys His Gln Tyr Leu Ile Thr Tyr Glu Asp  
1125 1130 1135

Asn Thr Ile Gly Gly Phe Ser Thr His Phe Asn Asn Tyr Leu Ile Glu  
1140 1145 1150

Asn Asn Tyr Ile Thr Lys His Asn Leu Tyr Val His Asn Ile Tyr Leu  
1155 1160 1165

Ser Asn Glu Pro Ile Glu His Ala Ser Phe Lys Asp Gln Gln Glu Val  
1170 1175 1180

Val Lys Met Asp Lys Cys Ser Leu Val Asn Arg Ile Lys Asn Tyr Leu  
1185 1190 1195 1200

Lys Asn Asn Pro Thr  
1205